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FIGURE 1

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1  ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGAGAGCGGCAGC 60
61  GGCTGCCAGGCTACGAGGAAGACCCCTTCCCGACTGCGGGGCTTGCGCTCCGGGACAA 120
121  GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGTGGAGGGAGCTCAGCTCGGTTG 180
181  TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT 240
241  CCCAATGCCAGCAACACCTCTGATGGCCCCGATAACCTCACTTCAGCAGGATCACCTCCT 300
301  CGCACGGGAGCATCTCCTACATCAACATCATGCTTCGGTGTTCGGCACCATCTGC 360
361  CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGCGGTCTCGTGAAGATCCAAAGCTG 420
421  CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC 480
481  TTTCTCCTGGGCATGCCCTTCATGATCCACCAGCTCATGGGCAATGGGGTGTGGCACTTT 540
541  GGGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCCAGCAC 600
601  TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTTCC 660
661  ACGAAGTTCCGGGAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCCCTCTCC 720
721  TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCCAGGAGGTGCA 780
781  GTGGGCTCGGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGGTTCACCCCTGTAC 840
841  CAGTTTTCCTGGCCCTTTGCCCTGCCCTTTTGTGGTCATCACAGCCGCATACGTGAGGATC 900
901  CTGCAGCGCATGACGTCCCTCAGTGGCCCCCGCCCTCCAGCGCAGCATCCGGCTGCGGGACA 960
961  AAGAGGTGACCCGACAGCCATCGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCC 1020
1021  TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCCGACCCCTCACCTTTGTCTAC 1080
1081  TTATACAAATGGGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC 1140
1141  ATCGTGCTCTGTGAGACGTTCCGGCAACAGCTTGGTCTGTCTGGTGAAGCCTGCAGCCAG 1200
1201  GGCAGCTTCGGCTGTTCAGCAACGCTCAGACGGCTGACGAGGAGGACAGAAAGCAAA 1260
1261  GGCACCTGA
```

FIGURE 2

[illegible]

FIGURE 3 **3/15**

1	M S V G A M K K G V G R A V G L G G G S	20
21	G C Q A T E E D P L P D C G A C A P G Q	40
41	G G R R W R L P Q P A W V E G S S A R L	60
61	W E Q A T G T G W M D L E A S L L P T G	80
81	P N A S N T S D G P D N L T S A G S P P	100
101	R T G S I S Y I N <u>I I M P S V E G T I C</u>	120
121	<u>L L G I I G N S T V I F A V V K K S K L</u>	140
141	H W C N N V P D <u>I F I I N L S V V D L L</u>	160
161	<u>F L L G M P F M I H Q L M G N G V W H F</u>	180
181	G E T M C T L I T A M D <u>A N S O F T S T</u>	200
201	<u>Y I L T A M A I D R Y L A T V H P I S S</u>	220
221	T K F R K P S <u>V A T L V I C L L W A L S</u>	240
241	<u>F I S I T P V W L Y A R L I P F P G G A</u>	260
261	<u>V G C G I R L P N P D T D L Y W F T L Y</u>	280
281	<u>O F F L A F A L P F V V I T A A Y V R I</u>	300
301	L Q R M T S S V A P A S Q R S I R L R T	320
321	K R <u>V T R T A I A I C L V F F V C W A P</u>	340
341	<u>Y Y V L O L T O L S I S R P T L T F V Y</u>	360
361	<u>L Y N A A I S L G Y A N S C L N P F V Y</u>	380
381	<u>I V L C E T F R K R L V L S V K P A A Q</u>	400
401	G Q L R A V S N A Q T A D E E R T E S K	420
421	G T	422

FIGURE 4

1 GCAGGGACCTGCACCGGCTGCATGGATCTGCAAAACCTCGTTGCTGTCCACTGGCCCCAA 60
 61 TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGTACCTCCTCGCAC 120
 121 AGGGAGTGCTCCTACATCAACATCATTTATGCCCTTCCGTGTTGGTACCATCTGTCTCCT 180
 181 GGGCATCGTGGGAAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG 240
 241 GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGGATCTGCTCTTCCT 300
 301 GCTGGGCATGCCCTTTTCATGATCCACAGCTCATGGGAAACGGCTCTGGCAGCTTTGGGA 360
 361 AACCATGTGCACCCCTCATCACAGCCATGGACGCCAACAGTCAGTTCACTAGCACCTACAT 420
 421 CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAA 480
 481 GTTCCGGAGCCCTCCATGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCGCTCTCCTTCAT 540
 541 CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTCCTTCCAGGGGTGCTGTGGG 600
 601 CTGTGGCATCCGCCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACCTGTACCAGTT 660
 661 TTTCCCTGGCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAAATACTACA 720
 721 GCGCATGACGCTTTCGGTGGCCCCAGCCTCCCAACGCAGCATCCGGCTTCGGACAAAAGAG 780
 781 GGTGACCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTGTGTGCTGGGCACCCCTACTA 840
 841 TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCCGACCCCTCACGTTTGTCTACTTGTA 900
 901 CAACGGGCCATCAGCTTGGGCTATGCTAACAGCTGCCCTGAACCCCTTTGTGTACATAGT 960
 961 GCTCTGTGAGACCTTTCGAAAACGCTTGGTGTGTGTCAGTGAAGCCTGCAGCCCCAGGGGCA 1020
 1021 GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGGACAGAAAGCAAAGGCAC 1080
 1081 CTGACAATTCCCCAGTCGCCCTCCAAGTCAGGCCACCCCATCAAAACCGTGGGGAGAGATAC 1140
 1141 TGAGATTAAACCCAAAGGCTACCTGGGAGAATGCAGAGGCTGGAGGCTGGGGGCTTGTAG 1200
 1201 CAACCACATTCCAC 1214

FIGURE 5

1	M	D	L	Q	T	S	L	P	F	K	V	S	G	N	A	M	R	T	Y	P	F	P	I	C	L	S	I	A	N	Y	R	Q
21	Q	D	N	L	T	L	G	T	G	K	V	H	T	M	G	Y	L	A	A	D	V	A	D	I	L	R	V	S	I	L	A	
41	I	I	M	P	S	V	G	I	P	K	V	S	F	N	C	I	L	I	T	P	V	S	A	P	F	W	L	C	S	N	R	
61	V	I	A	P	V	V	K	C	L	S	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
81	F	I	N	A	V	S	V	L	H	K	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
101	H	Q	L	M	G	N	V	L	F	G	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
121	A	M	A	N	S	V	F	T	Y	T	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
141	R	Y	A	A	V	V	F	T	Y	T	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
161	T	L	V	I	C	L	P	F	W	F	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
181	Y	A	R	L	I	P	L	F	W	F	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
201	P	D	T	D	L	Y	A	W	F	W	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
221	F	V	V	I	T	A	A	I	W	A	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
241	P	A	S	Q	R	S	I	R	W	I	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
261	I	C	L	V	F	F	R	C	A	P	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
281	S	I	S	R	P	T	T	P	Y	L	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
301	Y	A	N	S	C	L	N	P	Y	L	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
321	R	L	V	L	S	V	F	A	Y	L	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R	
341	Q	T	A	D	E	E	R	T	G	G	T	V	H	T	A	M	I	L	A	D	V	A	D	I	L	R	V	S	I	L	A	R

FIGURE 6

IP release in MCH1- and
mock-transfected Cos-7 cells

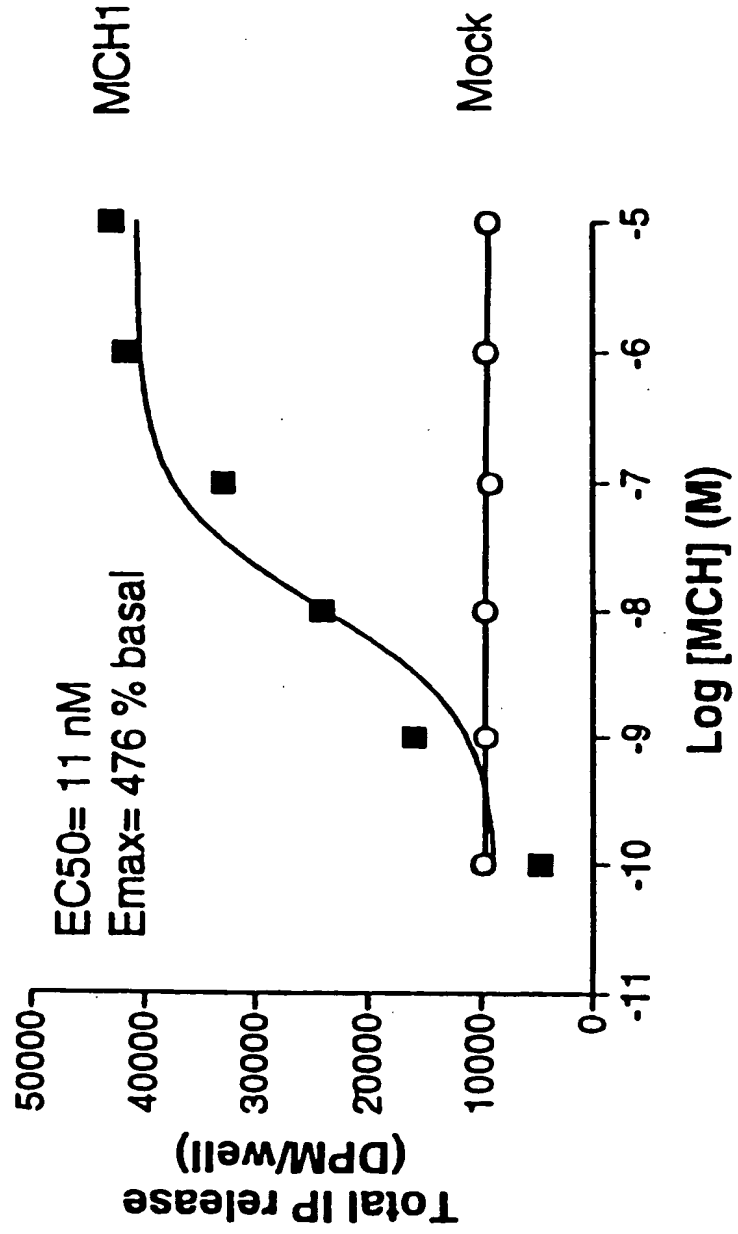


FIGURE 7A

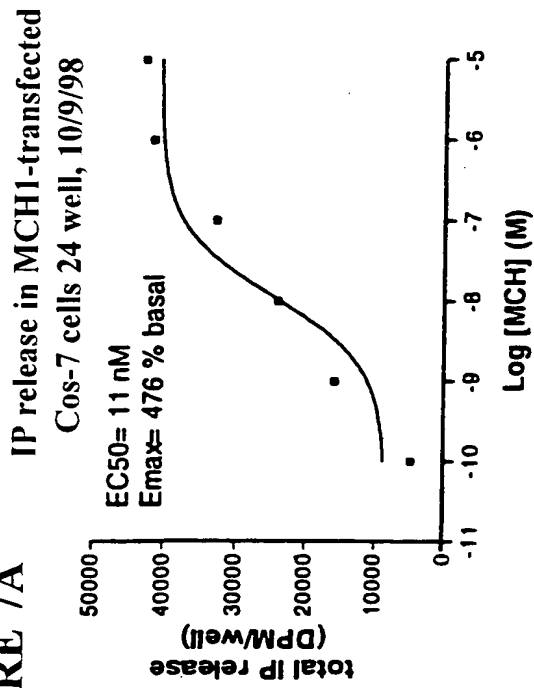


FIGURE 7B

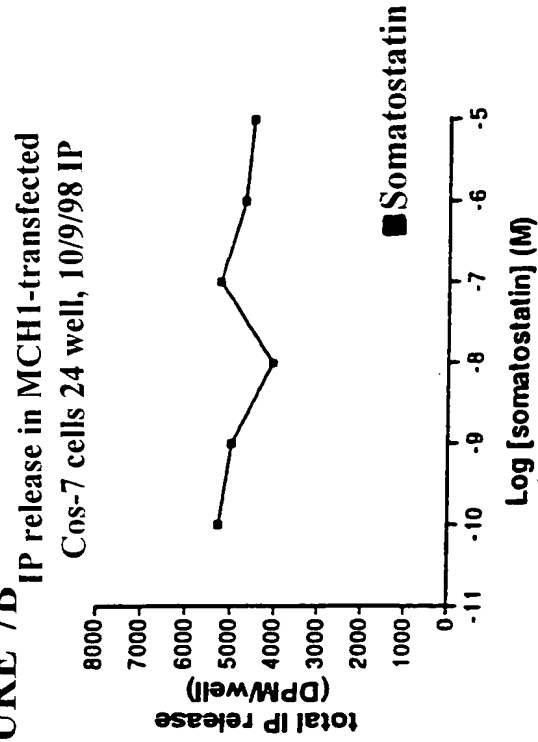


FIGURE 7C

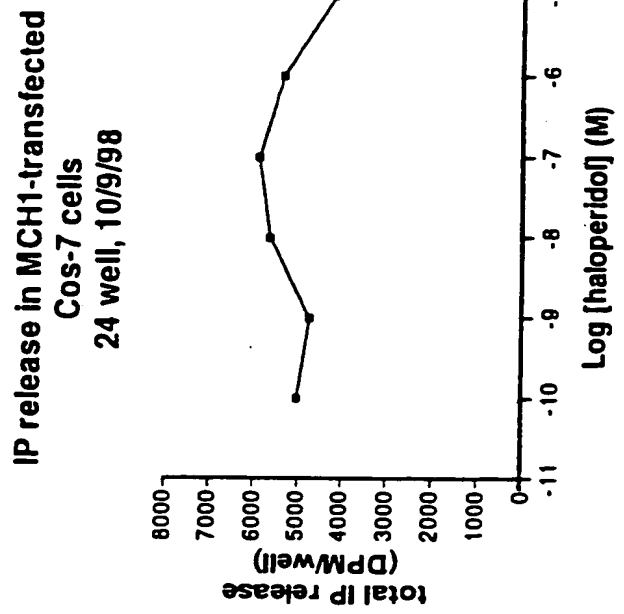
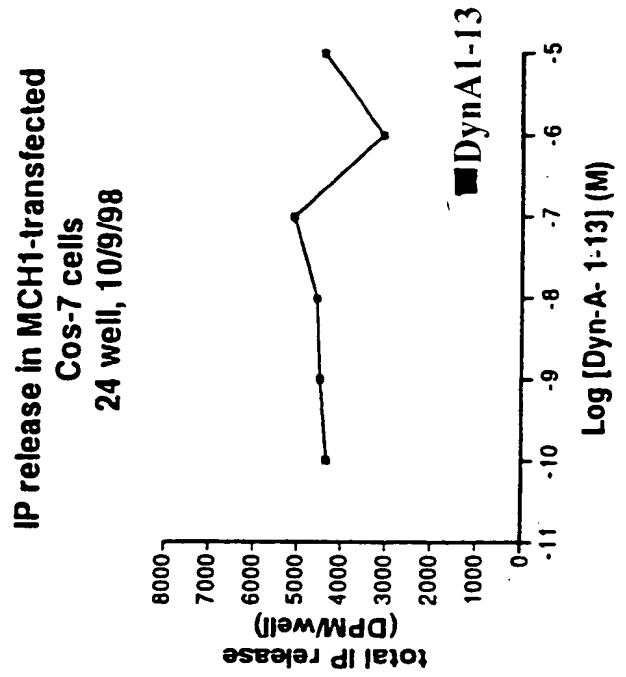


FIGURE 7D



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FIGURE 8A

Microphysiometer Response
CHO cells

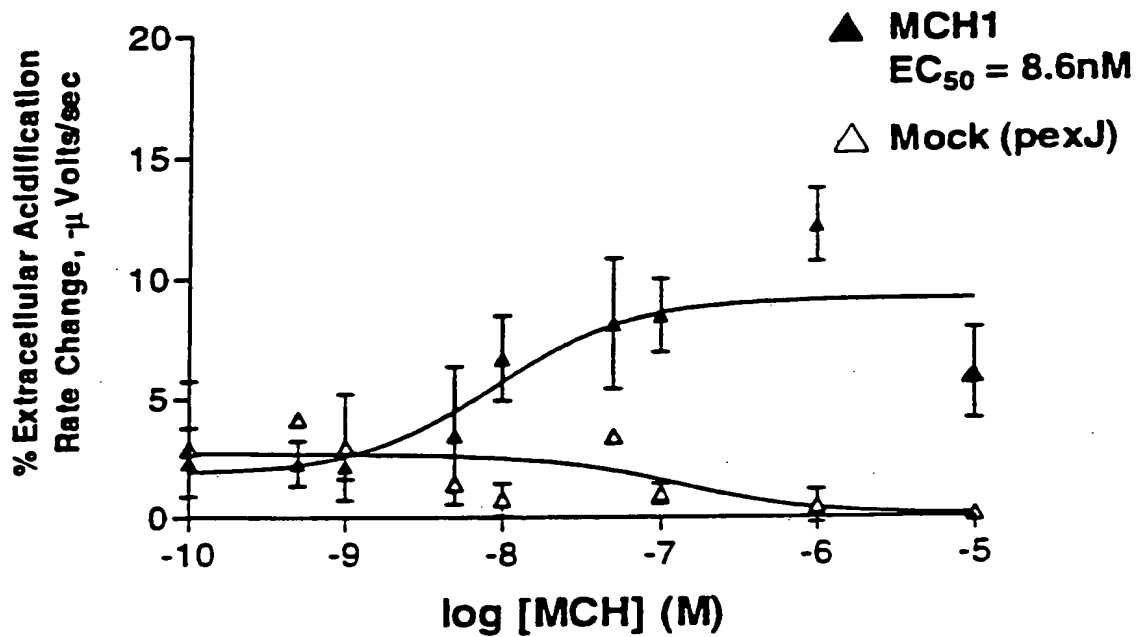
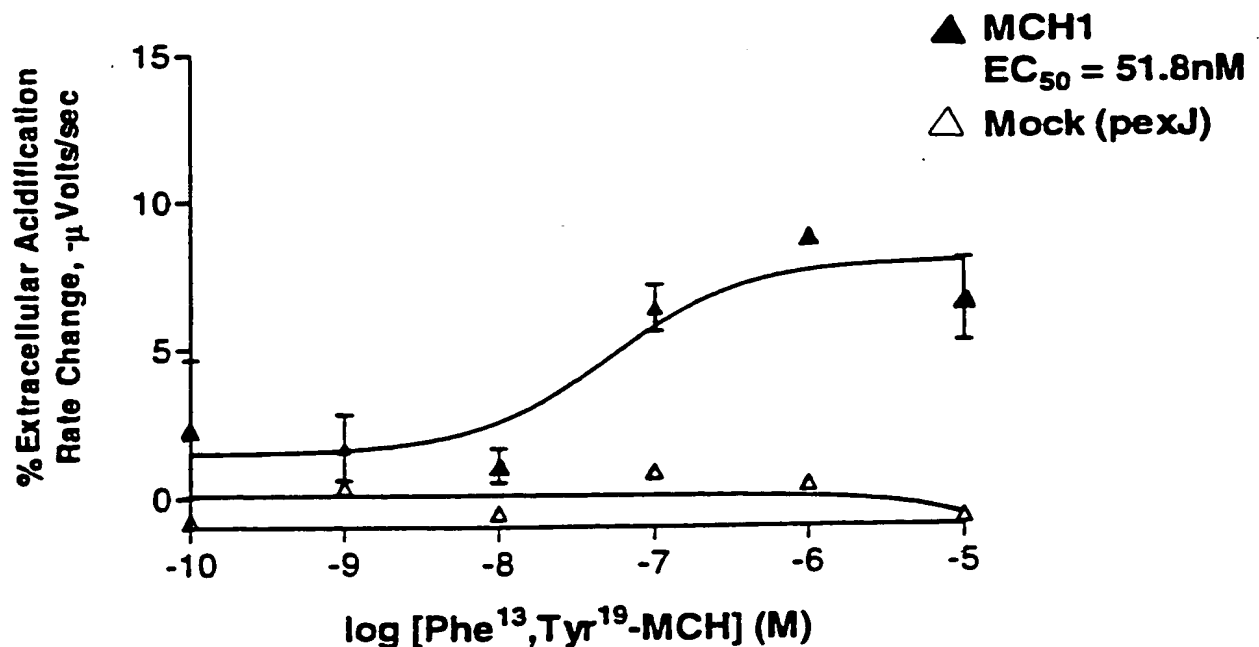


FIGURE 8B

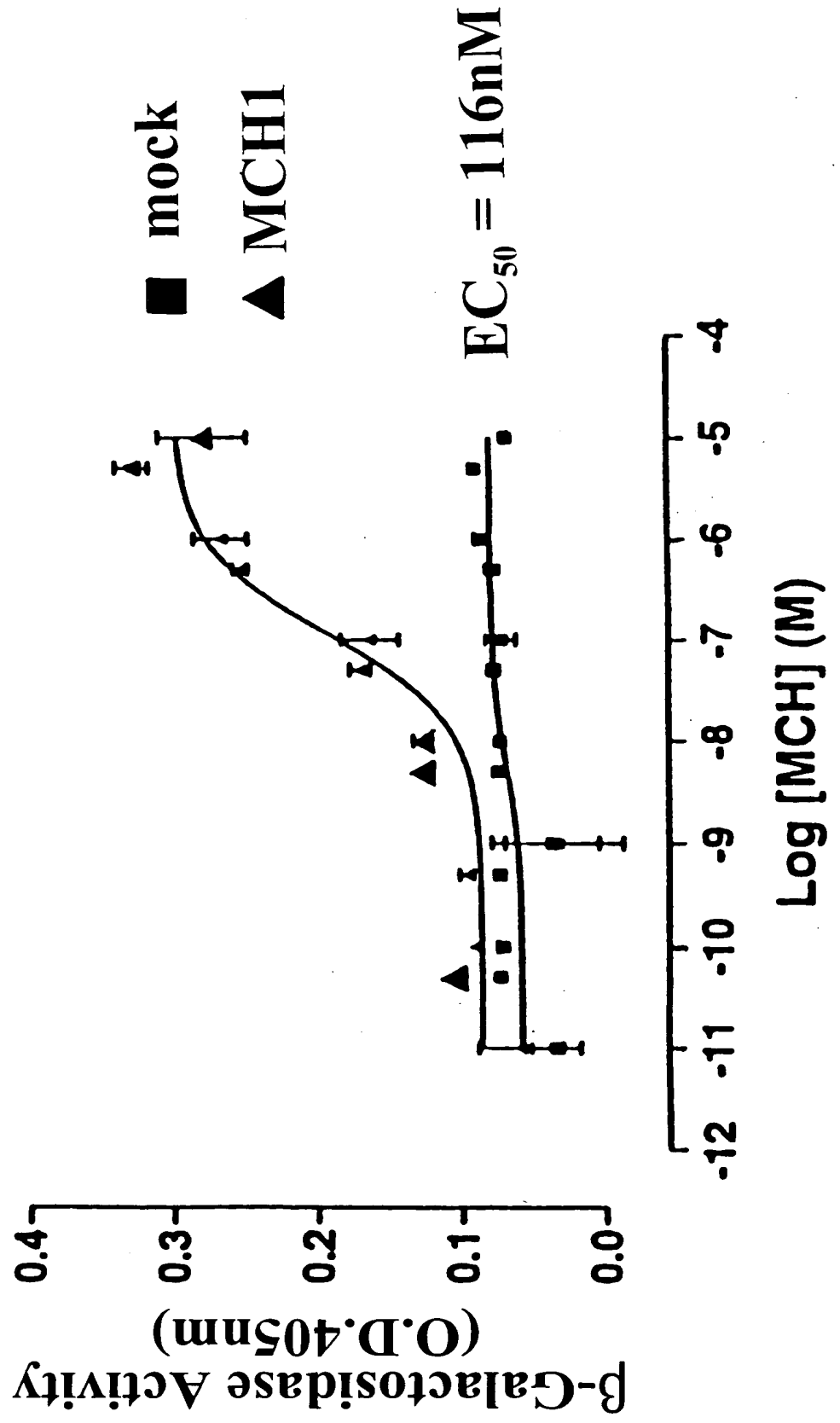
Microphysiometer Response
CHO cells



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FIGURE 9

Agonist-Mediated c-fos- β -gal
Activity in Cos-7 Cells



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FIGURE 10A

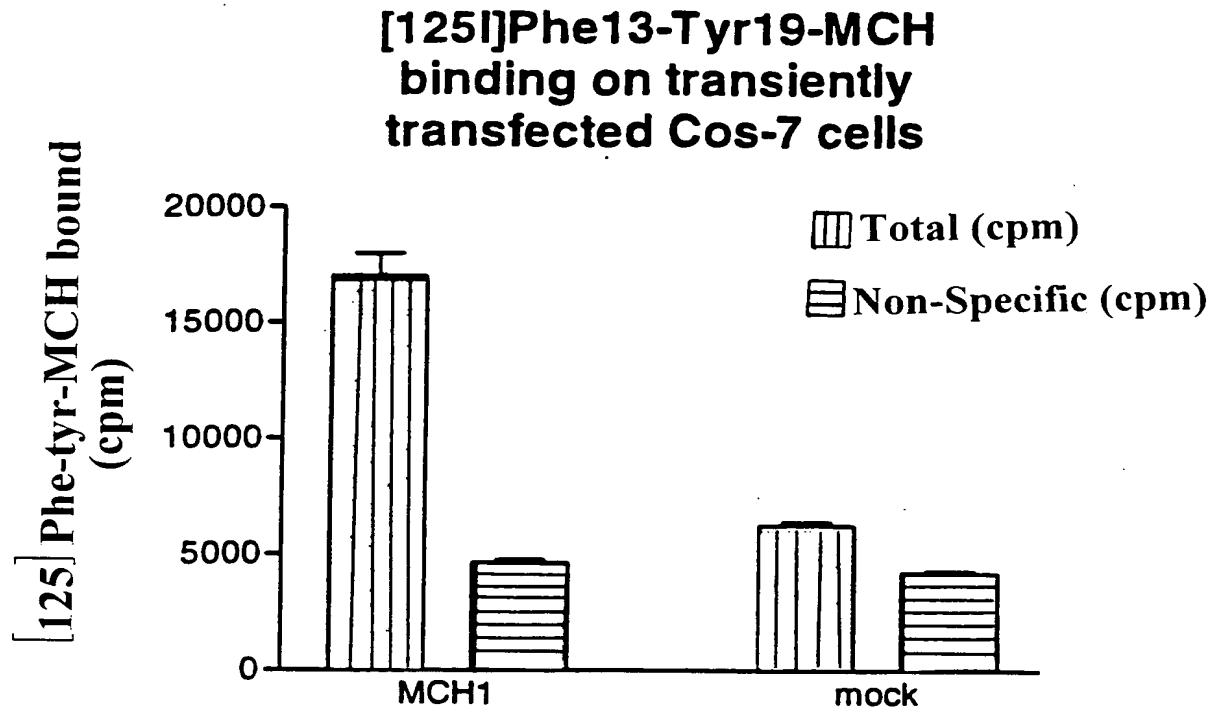
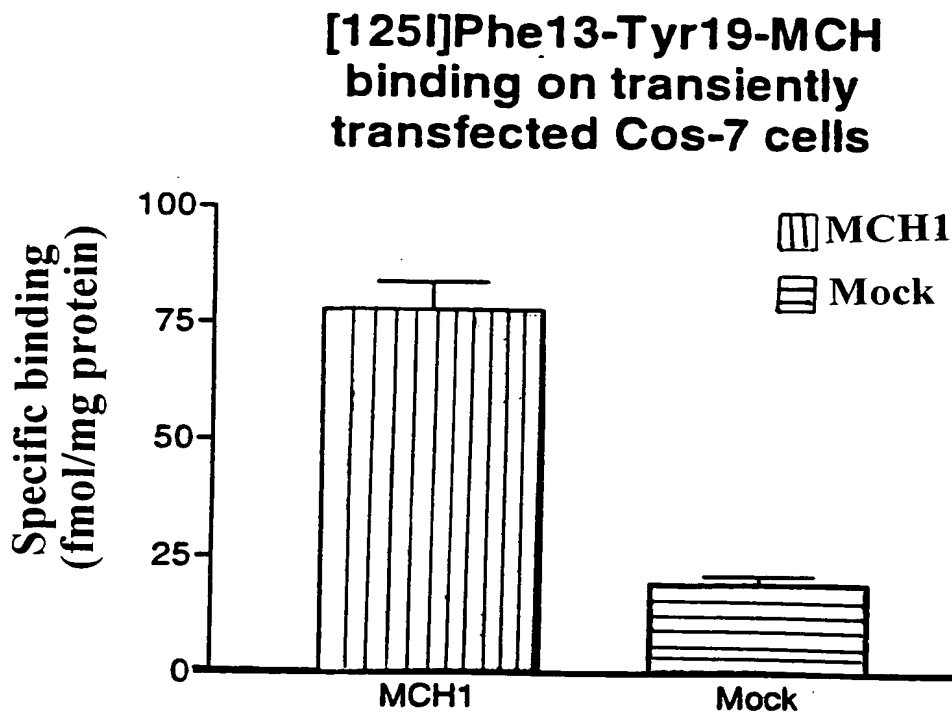


FIGURE 10B



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FIGURE 11

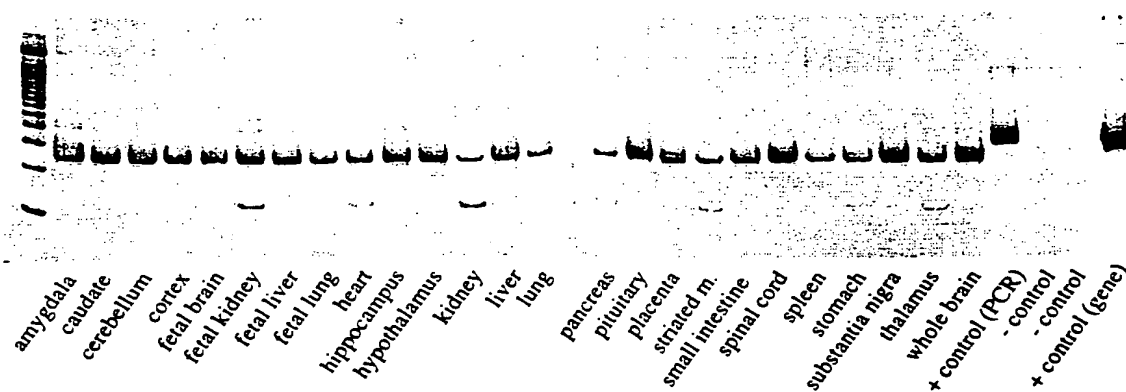


FIGURE 12

				1				40
TL231	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ				
R106	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ				
R114	MSVGAaKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ				
BO120	~~~~~	~~~~~	~~~~~	~~~~~				

				41				80
TL231	GRRRWRLPQP	AWVEGSSARL	WEQATGTGWM	DLEASLLPTG				
R106	GRRRWRLPQP	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG				
R114	GRRRWRLPQP	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG				
BO120	~~~~~	~~~~~	~~~~~M	DLEASLLPTG				

				81				100
TL231	PNASNTSDGP	DNLTSAGSPP...						
R106	PNASNTSDGP	DNLTSAGSPP...						
R114	PNASNTSDGP	DNLTSAGSPP...						
BO120	PNASNTSDGP	DNLTSAGSPP...						

FIGURE 13

[illegible]

FIGURE 14

[illegible]

FIGURE 15

1	M	D	L	E	A	S	L	G	P	T	G	P	R	L	H	F	L	G	C	N	G	M	T	R	I	S	C	F	R	V	V	N	L	C	R	A	S	I	I	N	M	P	T	A	M	P	S	V	L	P	N	S	Y	N	D	I	G	20
21	P	D	N	L	P	S	V	V	K	V	V	G	V	V	F	T	S	S	L	A	G	T	V	L	P	F	F	Y	R	V	L	C	I	P	L	I	D	A	V	W	L	P	N	S	I	N	T	I	40									
41	I	I	M	P	A	V	L	S	G	N	S	V	H	L	F	P	A	G	T	V	L	C	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	60												
61	V	I	I	F	A	V	L	S	G	N	S	V	H	L	F	P	A	G	T	V	L	C	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	80												
81	F	I	I	N	M	L	G	N	S	V	H	L	F	P	A	G	T	V	L	C	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	100														
101	H	Q	L	M	A	N	T	C	L	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	120																									
121	A	M	D	A	N	T	C	L	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	140																										
141	R	Y	L	A	N	T	C	L	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	160																										
161	T	L	V	I	C	L	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	180																												
181	Y	A	R	L	I	C	L	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	200																											
201	P	D	V	I	C	L	I	P	L	Y	A	R	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	220																												
221	F	V	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	240																																						
241	P	A	S	Q	V	R	F	P	T	L	N	K	P	P	E	S	K	G	T	260																																						
261	I	C	L	S	R	F	P	T	L	N	K	P	P	E	S	K	G	T	280																																							
281	S	I	S	R	F	P	T	L	N	K	P	P	E	S	K	G	T	300																																								
301	Y	A	N	S	L	S	E	R	320																																																	
321	R	L	V	L	S	E	R	340																																																		
341	Q	T	A	D	E	R	353																																																			